

FIG. 1 A-D

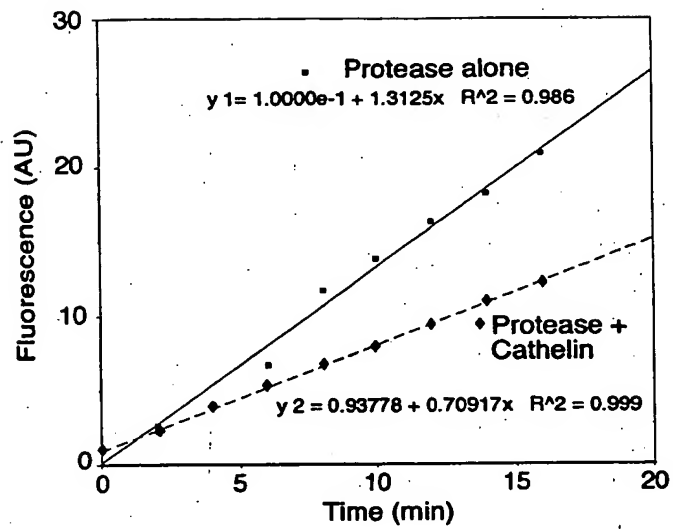


FIG. 2

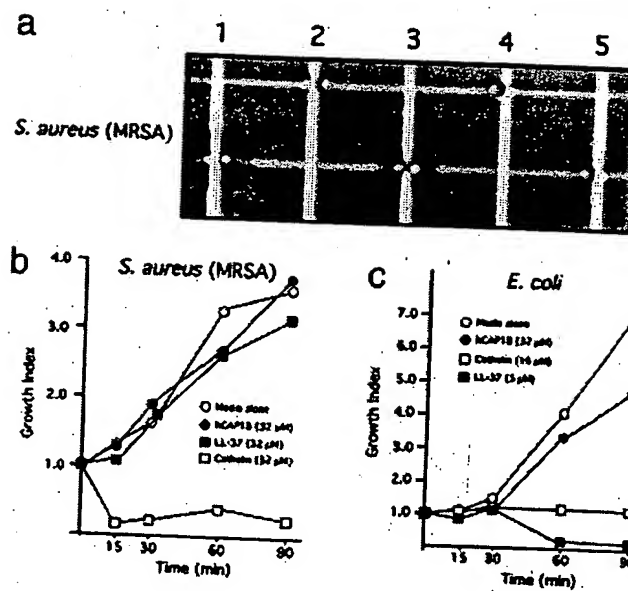


FIG. 3A-C

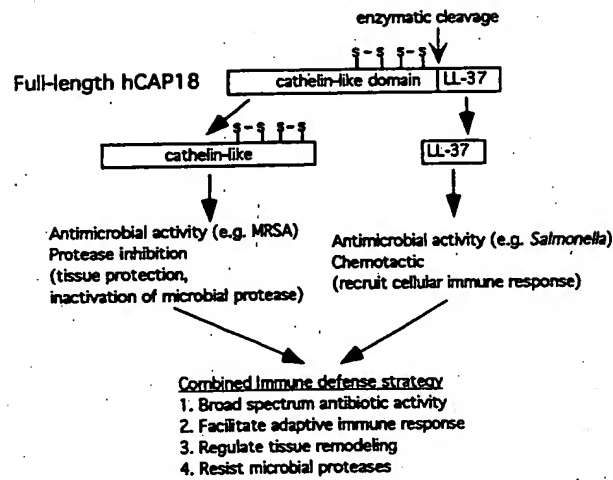


FIG. 4

## Formatted Alignments

FL Dog Cath Protein Met-Stop  
PR-39 cDNA Translation  
Il37 full length  
cramp full length  
Goat Cath-P82018 Bactenecin 5

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      10      20      30
METQKDSPLSLGRWSLLELLGLVITPAAS-S
METQRA SLCLGRWSLWLELLALVVPSSAS-A
MKTQRNGHSLGRWSLVLELLGLVMPLAIIA
MQFQRDVP SLWLWRSLSLELLGLGFSQ--
METQGA SLSLGRWSLWLELLGLVVPPLAS-A
METQRS SLGRWSLLELLGLVPAPAA

```

FL Dog Cath Protein Met-Stop  
PR-39 cDNA Translation  
Il37 full length  
cramp full length  
Goat Cath-P82018 Bactenecin 5

```

      40      50      60
RALSYREAVLRAVNGFNQRSSEENLYRLLEQ
QALSYREAVLRAVDRLNEQSSSEANLYRLLE
QVLSYKEAVLRAIDGINQRSSDANLYRLLD
-TPSYRDAVLRAVDDFNQQLDTNLYRLLD
QALSYREAVLRAVGQLNERSSSEANLYRLLE
QALSYREAVLRAVDNQRSSEANLYRLLE

```

FL Dog Cath Protein Met-Stop  
PR-39 cDNA Translation  
Il37 full length  
cramp full length  
Goat Cath-P82018 Bactenecin 5

```

      70      80      90
LNSQPKGDEDPNIPKPVSFETVKETVCPKTT
LDQP PKADEDPGTPKPVSFETVKETVCPRTT
LDP RP TMDGDPDTPKPVSFETVKETVCPRTT
LDP EPQGDEDPDTPKSVRF RVKETVCGKAE
LDP APND EVDPGTRKPVSFETVKETVCPRTT
LDP P DEDP TPKPVSFETVKETVCPRTT

```

FL Dog Cath Protein Met-Stop  
PR-39 cDNA Translation  
Il37 full length  
cramp full length  
Goat Cath-P82018 Bactenecin 5

```

      100      110      120
QQPLEQCGFKDNLGLVKQCE GTVILDEDTGY
RQPPEL CDFKENGRV KQC VGTVTLNPSIHS
QQSPED CDFK K DGLVKRCMGTVTLNQARGS
RQLPEQCA FKEQGVVKQCMGA VTENPAADS
QQPPEE CDFKENGLVKQCV GTVTLDPSNDQ
QQPPE CDFKENGLVKQCV GTVTLNPS

```

FL Dog Cath Protein Met-Stop  
PR-39 cDNA Translation  
Il37 full length  
cramp full length  
Goat Cath-P82018 Bactenecin 5

```

      130      140      150
FDLNCDS - - ILQVKKIDR - - LKE LIT TGAQ
LDISCNE - - IQSVRR RP - - RPPYL RP RP
FDISC DK - - DNKR FAL LG - - DFFR KSKE
FDISCNEPGAQP FRF K KIS RLAGLLR KGGE
FDINCNE - - LQS SVRF RPPI RRPPI RP - PFN
FDISCNEPG Q VR R

```

FL Dog Cath Protein Met-Stop  
PR-39 cDNA Translation  
Il37 full length  
cramp full length  
Goat Cath-P82018 Bactenecin 5

```

      160      170      180
KIGKKIRRIGQRIKD FLKNLQPR - - EEKS*
PPFFPP RLPPRI PP GFPPRFPPPR - - FPGKR
KIGKEFKRIVQRIKD FLRN LVPRTES
KIGEKL K KIGQKIKN EFQK LV PQ - - PEQ
PPFRPP VRPPFRPPFRPPFRPPPIGPFPGR R
KIG R I QRIK F L PR R

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FIG.5